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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/625,202

DATE: 08/31/2004

TIME: 15:07:15

Input Set : A:\89DIV.ST25.txt

Output Set: N:\CRF4\08312004\J625202.raw

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3 <110> APPLICANT: Figdor, Carl Gustav
4      Geijtenbeek, Teunis Bernard Herman
5      Van Kooyk, Yvette
6      Torensma, Ruurd
8 <120> TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING DENDRITIC CELL-T CELL
9      INTERACTION
11 <130> FILE REFERENCE: 89 DIV
13 <140> CURRENT APPLICATION NUMBER: US 10/625,202
14 <141> CURRENT FILING DATE: 2003-07-23
16 <150> PRIOR APPLICATION NUMBER: 09/719,961
17 <151> PRIOR FILING DATE: 2001-09-24
19 <150> PRIOR APPLICATION NUMBER: PCT/NL00/00253
20 <151> PRIOR FILING DATE: 2000-04-19
22 <150> PRIOR APPLICATION NUMBER: US 60/176,924
23 <151> PRIOR FILING DATE: 2000-01-20
25 <150> PRIOR APPLICATION NUMBER: EP 99201204.7
26 <151> PRIOR FILING DATE: 1999-04-19
28 <160> NUMBER OF SEQ ID NOS: 2
30 <170> SOFTWARE: PatentIn version 3.2
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1215
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (1)..(1215)
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45 1          5          10          15
47 gag gaa cag ctg aga ggc ctt gga ttc cga cag act cga gga tac aag      96
48 Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys
49          20          25          30
51 agc tta gca ggg tgt ctt ggc cat ggt ccc ctg gtg ctg caa ctc ctc      144
52 Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu
53          35          40          45
55 tcc ttc acg ctc ttg gct ggg ctc ctt gtc caa gtg tcc aag gtc ccc      192
56 Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro
57          50          55          60
59 agc tcc ata agt cag gaa caa tcc agg caa gac gcg atc tac cag aac      240
60 Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn
61 65          70          75          80
63 ctg acc cag ctt aaa gct gca gtg ggt gag ctc tca gag aaa tcc aag      288

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64	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Ser	Glu	Lys	Ser	Lys	
65					85					90				95			
67	ctg	cag	gag	atc	tac	cag	gag	ctg	acc	cag	ctg	aag	gct	gca	gtg	ggt	336
68	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly	
69				100					105					110			
71	gag	ctt	cca	gag	aaa	tct	aag	ctg	cag	gag	atc	tac	cag	gag	ctg	acc	384
72	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	
73				115					120					125			
75	cgg	ctg	aag	gct	gca	gtg	ggt	gag	ctt	cca	gag	aaa	tct	aag	ctg	cag	432
76	Arg	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln	
77		130					135						140				
79	gag	atc	tac	cag	gag	ctg	acc	tgg	ctg	aag	gct	gca	gtg	ggt	gag	ctt	480
80	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Trp	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	
81	145				150					155					160		
83	cca	gag	aaa	tct	aag	atg	cag	gag	atc	tac	cag	gag	ctg	act	cgg	ctg	528
84	Pro	Glu	Lys	Ser	Lys	Met	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Arg	Leu	
85				165					170					175			
87	aag	gct	gca	gtg	ggt	gag	ctt	cca	gag	aaa	tct	aag	cag	cag	gag	atc	576
88	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Gln	Gln	Glu	Ile	
89				180					185					190			
91	tac	cag	gag	ctg	acc	cgg	ctg	aag	gct	gca	gtg	ggt	gag	ctt	cca	gag	624
92	Tyr	Gln	Glu	Leu	Thr	Arg	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	
93				195					200					205			
95	aaa	tct	aag	cag	cag	gag	atc	tac	cag	gag	ctg	acc	cgg	ctg	aag	gct	672
96	Lys	Ser	Lys	Gln	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Arg	Leu	Lys	Ala	
97		210					215						220				
99	gca	gtg	ggt	gag	ctt	cca	gag	aaa	tct	aag	cag	cag	gag	atc	tac	cag	720
100	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Gln	Gln	Glu	Ile	Tyr	Gln	
101	225				230					235				240			
103	gag	ctg	acc	cag	ctg	aag	gct	gca	gtg	gaa	cgc	ctg	tgc	cac	ccc	tgt	768
104	Glu	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Glu	Arg	Leu	Cys	His	Pro	Cys	
105				245					250					255			
107	ccc	tgg	gaa	tgg	aca	ttc	ttc	caa	gga	aac	tgt	tac	ttc	atg	tct	aac	816
108	Pro	Trp	Glu	Trp	Thr	Phe	Phe	Gln	Gly	Asn	Cys	Tyr	Phe	Met	Ser	Asn	
109				260					265					270			
111	tcc	cag	cgg	aac	tgg	cac	gac	tcc	atc	acc	gcc	tgc	aaa	gaa	gtg	ggg	864
112	Ser	Gln	Arg	Asn	Trp	His	Asp	Ser	Ile	Thr	Ala	Cys	Lys	Glu	Val	Gly	
113				275					280					285			
115	gcc	cag	ctc	gtc	gta	atc	aaa	agt	gct	gag	gag	cag	aac	ttc	cta	cag	912
116	Ala	Gln	Leu	Val	Val	Ile	Lys	Ser	Ala	Glu	Glu	Gln	Asn	Phe	Leu	Gln	
117		290					295					300					
119	ctg	cag	tct	tcc	aga	agt	aac	cgc	ttc	acc	tgg	atg	gga	ctt	tca	gat	960
120	Leu	Gln	Ser	Ser	Arg	Ser	Asn	Arg	Phe	Thr	Trp	Met	Gly	Leu	Ser	Asp	
121	305				310					315				320			
123	cta	aat	cag	gaa	ggc	acg	tgg	caa	tgg	gtg	gac	ggc	tca	cct	ctg	ttg	1008
124	Leu	Asn	Gln	Glu	Gly	Thr	Trp	Gln	Trp	Val	Asp	Gly	Ser	Pro	Leu	Leu	
125				325					330					335			
127	ccc	agc	ttc	aag	cag	tat	tgg	aac	aga	gga	gag	ccc	aac	aac	gtt	ggg	1056
128	Pro	Ser	Phe	Lys	Gln	Tyr	Trp	Asn	Arg	Gly	Glu	Pro	Asn	Asn	Val	Gly	

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129          340          345          350
131 gag gaa gac tgc gcg gaa ttt agt ggc aat ggc tgg aac gac gac aaa      1104
132 Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys
133          355          360          365
135 tgt aat ctt gcc aaa ttc tgg atc tgc aaa aag tcc gca gcc tcc tgc      1152
136 Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys
137          370          375          380
139 tcc agg gat gaa gaa cag ttt ctt tct cca gcc cct gcc acc cca aac      1200
140 Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn
141 385          390          395          400
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144 Pro Pro Pro Ala
148 <210> SEQ ID NO: 2
149 <211> LENGTH: 404
150 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
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159 Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys
160          20          25          30
163 Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu
164          35          40          45
167 Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro
168          50          55          60
171 Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn
172 65          70          75          80
175 Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys
176          85          90          95
179 Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly
180          100          105          110
183 Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
184          115          120          125
187 Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
188          130          135          140
191 Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu
192 145          150          155          160
195 Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
196          165          170          175
199 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile
200          180          185          190
203 Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
204          195          200          205
207 Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala
208          210          215          220
211 Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln
212 225          230          235          240
215 Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys
216          245          250          255

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219 Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn
220           260           265           270
223 Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly
224           275           280           285
227 Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln
228           290           295           300
231 Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp
232 305           310           315           320
235 Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu
236           325           330           335
239 Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly
240           340           345           350
243 Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys
244           355           360           365
247 Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys
248           370           375           380
251 Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn
252 385           390           395           400
255 Pro Pro Pro Ala

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VERIFICATION SUMMARY

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